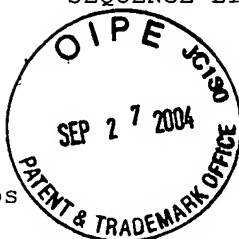


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<110> Pompejus, Markus
 Seulberger, Harald
 Hoeffken, Hans Wolfgang
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Val Leu Val Gly	Asp Val Ala Asp Lys	Ser Cys Ile Ile	Val Asp Asp			
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Glu Asn Cys Ala	Lys Glu Val Ile Ala	Ile Val Thr His	Gly Ile Phe			
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Val Ser Thr Asn	Thr Val Pro Val Asp	Leu Asn Leu Asp	Ile Tyr His			
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Gln Ile Asp Ile	Ser Ala Ile Leu Ala	Glu Ala Ile Arg	Arg Leu His			
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Tyr	Asn	Arg	Thr	Val	Glu	Glu	Ile	Thr	Ala	Glu	Leu	Gly	Cys	Asp	Arg	
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GTC	ATC	TAT	CAA	TCT	TTG	GAT	GAC	CTC	ATC	GAC	TGT	TGC	AAG	ACA	GAC	3134
Val	Ile	Tyr	Gln	Ser	Leu	Asp	Asp	Leu	Ile	Asp	Cys	Cys	Lys	Thr	Asp	
				445					450					455		
ATC	ATC	TCA	GAA	TTT	GAA	GTT	GGA	GTT	TTC	ACT	GGT	AAC	TAC	GTT	ACA	3182
Ile	Ile	Ser	Glu	Phe	Glu	Val	Gly	Val	Phe	Thr	Gly	Asn	Tyr	Val	Thr	
			460					465					470			
GGT	GTT	GAG	GAT	GTG	TAC	TTG	CAG	GAA	TTA	GAA	CGT	TGC	CGC	GCT	CTT	3230
Gly	Val	Glu	Asp	Val	Tyr	Leu	Gln	Glu	Leu	Glu	Arg	Cys	Arg	Ala	Leu	
		475					480					485				
AAT	AAC	TCG	AAT	AAG	GGT	GAA	GCG	AAG	GCC	GAG	GTT	GAT	ATT	GGT	CTC	3278
Asn	Asn	Ser	Asn	Lys	Gly	Glu	Ala	Lys	Ala	Glu	Val	Asp	Ile	Gly	Leu	
490						495					500					

TAC AAT TCT GCC GAC TAT TAGCGGCGCC GTTGCCGGCA TCCGGCCCCA	3326
Tyr Asn Ser Ala Asp Tyr	
505 510	
TATATAGACT CATCGGGACC TAAAATAAGC CTTTACAGAT CATTATCTAC AAATATAGAT	3386
ACCATTAATA GCCTGACTTT CGACTTACTC CTAGCACACC CCGTTGTATC CCTGTGCTTG	3446
CTTTCTTAAA TGCCGTTGGT TAGGCTTTGG ACTTAGCGTC CCGCCCATTT TCTAGCATGT	3506
GCAGATCTAG CAAATTTGGC CTAAGACAAG AAGATCCATT CGGCACCCAC ATCCTGGAGC	3566
CAGCACACAG TGGACCCAGA C ATG AGC AGC GGC AAT ATA TGG AAG CAA TTG	3617
Met Ser Ser Gly Asn Ile Trp Lys Gln Leu	
1 5 10	
CTA GAG GAG AAT AGC GAA CAG CTG GAC CAG TCC ACT ACG GAG ACT TAC	3665
Leu Glu Glu Asn Ser Glu Gln Leu Asp Gln Ser Thr Thr Glu Thr Tyr	
15 20 25	
GTG GTA TGC TGC GAG AAC GAA GAT TCC CTT AAC CAG TTT TTG CAA CAA	3713
Val Val Cys Cys Glu Asn Glu Asp Ser Leu Asn Gln Phe Leu Gln Gln	
30 35 40	
TGT TGG CAG ATT GAC GAG GGC GAG AAG GTG ACC AAC CTG GAG CCG TTG	3761
Cys Trp Gln Ile Asp Glu Gly Glu Lys Val Thr Asn Leu Glu Pro Leu	
45 50 55	
GGA TTC TTT ACA AAG GTG GTT TCG CGC GAC GAA GAG AAC CTC CGG CTC	3809
Gly Phe Phe Thr Lys Val Val Ser Arg Asp Glu Glu Asn Leu Arg Leu	
60 65 70	
AAC GTA TAC TAT GCC AAG AGC CCA CTG GAT GCA CAG ACG CTG CAG TTT	3857
Asn Val Tyr Tyr Ala Lys Ser Pro Leu Asp Ala Gln Thr Leu Gln Phe	
75 80 85 90	
CTG GGC GTG TTC CTG CGC CAA ATG GAA ACC TCA CAA ATA CGT TGG ATC	3905
Leu Gly Val Phe Leu Arg Gln Met Glu Thr Ser Gln Ile Arg Trp Ile	
95 100 105	
TTC CTA CTG GAC TGG CTG CTA GAC GAT AAA CGA TTA TGG CTA CGT CAA	3953
Phe Leu Leu Asp Trp Leu Leu Asp Asp Lys Arg Leu Trp Leu Arg Gln	
110 115 120	
CTG CGG AAC TCG TGG GCC GCC TTG GAG GAA GCG CAG GTG GCA CCC TTT	4001
Leu Arg Asn Ser Trp Ala Ala Leu Glu Glu Ala Gln Val Ala Pro Phe	
125 130 135	
CCA GGT GGC GCT GTG GTG GTG GTC CTC AAC CCG AGT CAC GTG ACA CAA	4049
Pro Gly Gly Ala Val Val Val Val Leu Asn Pro Ser His Val Thr Gln	
140 145 150	
CTG GAG CGA AAC ACG ATG GTT TGG AAC TCC CGC CGT CTG GAC CTG GTA	4097
Leu Glu Arg Asn Thr Met Val Trp Asn Ser Arg Arg Leu Asp Leu Val	
155 160 165 170	
CAC CAG ACA CTG CGA GCT GCA TGC CTC AAC ACC GGC TCG GCG CTA GTT	4145
His Gln Thr Leu Arg Ala Ala Cys Leu Asn Thr Gly Ser Ala Leu Val	
175 180 185	

ACA CTT GAT CCT AAT ACT GCG CGC GAA GAC GTC ATG CAC ATA TGT GCG	4193
Thr Leu Asp Pro Asn Thr Ala Arg Glu Asp Val Met His Ile Cys Ala	
190 195 200	
CTG CTT GCG GGG CTG CCT ACA TCC CGT CCC GTC GCG ATG CTA AGC CTG	4241
Leu Leu Ala Gly Leu Pro Thr Ser Arg Pro Val Ala Met Leu Ser Leu	
205 210 215	
CAA AGT CTA TTC ATC CCC CAC GGT GCA GAT TCC ATC GGC AAG ATC TGC	4289
Gln Ser Leu Phe Ile Pro His Gly Ala Asp Ser Ile Gly Lys Ile Cys	
220 225 230	
ACC ATC GCG CCC GAG TTC CCT GTT GCT ACG GTG TTC GAC AAC GAT TTT	4337
Thr Ile Ala Pro Glu Phe Pro Val Ala Thr Val Phe Asp Asn Asp Phe	
235 240 245 250	
GTG AGC TCG ACA TTC GAG GCC GCA ATT GCT CCA GAA CTT ACT CCA GGA	4385
Val Ser Ser Thr Phe Glu Ala Ala Ile Ala Pro Glu Leu Thr Pro Gly	
255 260 265	
CCA CGT GTG CCA TCT GAC CAC CCA TGG CTA ACA GAG CCT ACC AAC CCC	4433
Pro Arg Val Pro Ser Asp His Pro Trp Leu Thr Glu Pro Thr Asn Pro	
270 275 280	
CCT TCG GAG GCA ACC GCT TGG CAT TTC GAT CTC CAA GGT CGC CTC GCT	4481
Pro Ser Glu Ala Thr Ala Trp His Phe Asp Leu Gln Gly Arg Leu Ala	
285 290 295	
ACC CTA TAC CGG CAT CTT GGT GAC TCT AAC AAG GCC ATA TCT GTT ACT	4529
Thr Leu Tyr Arg His Leu Gly Asp Ser Asn Lys Ala Ile Ser Val Thr	
300 305 310	
CAG CAC CGC TTC CAC AAG CCC CGC TCG GAA GAT TAT GCA TAC GAA TTC	4577
Gln His Arg Phe His Lys Pro Arg Ser Glu Asp Tyr Ala Tyr Glu Phe	
315 320 325 330	
GAG CTG CCG TCT AAG CAC CCT ACA ATA CGT GAC CTC ATA CGC TCT GCC	4625
Glu Leu Pro Ser Lys His Pro Thr Ile Arg Asp Leu Ile Arg Ser Ala	
335 340 345	
GCA GCC GAC TCA CCG AAC GAC GTC GCT GAC TCC ATC GAT GGG CTT ATG	4673
Ala Ala Asp Ser Pro Asn Asp Val Ala Asp Ser Ile Asp Gly Leu Met	
350 355 360	
GAT GGT ATC GTA CAA AGG AAT GTT CAT TGACGTCGAC ACAAAAAATTT	4720
Asp Gly Ile Val Gln Arg Asn Val His	
365 370	
TGTTACTGTT CTCTCGAGAA CTATTCTCAT CCAGTACTGA CATATTAGAA GGCGAAGTGA	4780
ACTAGGATTT ATATAAAGTA GCCTTCAGGC AATTGCACAG GGTCTATTGA GTCGCTGCCG	4840
TTCACGAGAG AGCCCAATAT ATCGAGGACT AATTGGTCAC TTTTGTTTTG CTATACTCAC	4900
CCTGTATTTG CTAATCATTT ATCCGCTTTG TCCAAGTGGT TGCGAAGATA TCGAGCCAGA	4960
ACATTAGAAT CTGGTTTGCC GCATCCTAGA GCTGTCTCCA AGCCAGTTGA ACCGTTGCGG	5020
GAGATTACCG CAGCCGGTTT GATCAGAGTA CTGGTGACTG CCAGCACCCA CGTTTGTGAC	5080

TTATAAATAT ACGCCCTGTG GAGCCATAGC CATTGGCATA AAGAGAAGAG CACCCCGTGC 5140
CACGATGCAG ACACTTCCGG TGTACCCAGC GTCACAGACT GCGTCGCCTA CGAAGCGTGA 5200
ACTTGCAGCG GCGCCCTCGG TGCCGCAGGA CGGCGCCCGG CTGCCTGCGC AGCTCACTTT 5260
AGTGACGCCC CCAGAACCTG ATATCCAGAA GAAGTCAGTG CGATCTCAGG TCGCGCGTTT 5320
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Leu Thr Tyr Gln Phe Gly Ala Ser Phe Ala Ala Ile Thr Phe Ser Thr
35 40 45
Met Leu Leu Tyr Ser Ile Phe Thr Phe Arg Thr Thr Ala Trp Arg Thr
50 55 60
Arg Phe Arg Arg Asp Ala Asn Lys Ala Asp Asn Lys Ala Ala Ser Val
65 70 75 80
Ala Leu Asp Ser Leu Ile Asn Phe Glu Ala Val Lys Tyr Phe Asn Asn
85 90 95
Glu Lys Tyr Leu Ala Asp Lys Tyr His Thr Ser Leu Met Lys Tyr Arg
100 105 110
Asp Ser Gln Ile Lys Val Ser Gln Ser Leu Ala Phe Leu Asn Thr Gly
115 120 125
Gln Asn Leu Ile Phe Thr Thr Ala Leu Thr Ala Met Met Tyr Met Ala
130 135 140
Cys Asn Gly Val Met Gln Gly Ser Leu Thr Val Gly Asp Leu Val Leu
145 150 155 160
Ile Asn Gln Leu Val Phe Gln Leu Ser Val Pro Leu Asn Phe Leu Gly
165 170 175
Ser Val Tyr Arg Asp Leu Lys Gln Ser Leu Ile Asp Met Glu Ser Leu
180 185 190
Phe Lys Leu Gln Lys Asn Gln Val Thr Ile Lys Asn Ser Pro Asn Ala
195 200 205
Gln Asn Leu Pro Ile His Lys Pro Leu Asp Ile Arg Phe Glu Asn Val
210 215 220

Thr Phe Gly Tyr Asp Pro Glu Arg Arg Ile Leu Asn Asn Val Ser Phe
 225 230 235 240
 Thr Ile Pro Ala Gly Met Lys Thr Ala Ile Val Gly Pro Ser Gly Ser
 245 250 255
 Gly Lys Ser Thr Ile Leu Lys Leu Val Phe Arg Phe Tyr Glu Pro Glu
 260 265 270
 Gln Gly Arg Ile Leu Val Gly Gly Thr Asp Ile Arg Asp Leu Asp Leu
 275 280 285
 Leu Ser Leu Arg Lys Ala Ile Gly Val Val Pro Gln Asp Thr Pro Leu
 290 295 300
 Phe Asn Asp Thr Ile Trp Glu Asn Val Lys Phe Gly Asn Ile Ser Ser
 305 310 315 320
 Ser Asp Asp Glu Ile Leu Arg Ala Ile Glu Lys Ala Gln Leu Thr Lys
 325 330 335
 Leu Leu Gln Asn Leu Pro Lys Gly Ala Ser Thr Val Val Gly Glu Arg
 340 345 350
 Gly Leu Met Ile Ser Gly Gly Glu Lys Gln Arg Leu Ala Ile Ala Arg
 355 360 365
 Val Leu Leu Lys Asp Ala Pro Leu Met Phe Phe Asp Glu Ala Thr Ser
 370 375 380
 Ala Leu Asp Thr His Thr Glu Gln Ala Leu Leu His Thr Ile Gln Gln
 385 390 395 400
 Asn Phe Ser Ser Asn Ser Lys Thr Ser Val Tyr Val Ala His Arg Leu
 405 410 415
 Arg Thr Ile Ala Asp Ala Asp Lys Ile Ile Val Leu Glu Gln Gly Ser
 420 425 430
 Val Arg Glu Glu Gly Thr His Ser Ser Leu Leu Ala Ser Gln Gly Ser
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 Leu Tyr Arg Gly Leu Trp Asp Ile Gln Glu Asn Leu Thr Leu Pro Glu
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 Arg Pro Glu Gln Ser Thr Gly Ser Gln His Ala
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<400> 5

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 Ala Pro Glu Leu Phe Asp Gly Ser Leu Phe Leu Gln His Arg Gly Gln

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Asp	Ala	Ala	Gly	Ile	Ala	Thr	Cys	Gly	Pro	Gly	Gly	Arg	Leu	Tyr	Gln
	35						40					45			
Cys	Lys	Gly	Asn	Gly	Met	Ala	Arg	Asp	Val	Phe	Thr	Gln	Ala	Arg	Met
	50					55					60				
Ser	Gly	Leu	Val	Gly	Ser	Met	Gly	Ile	Ala	His	Leu	Arg	Tyr	Pro	Thr
	65					70					75				80
Ala	Gly	Ser	Ser	Ala	Asn	Ser	Glu	Ala	Gln	Pro	Phe	Tyr	Val	Asn	Ser
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Pro	Tyr	Gly	Ile	Cys	Met	Ser	His	Asn	Gly	Asn	Leu	Val	Asn	Thr	Met
			100					105					110		
Ser	Leu	Arg	Arg	Tyr	Leu	Asp	Glu	Asp	Val	His	Arg	His	Ile	Asn	Thr
	115					120					125				
Asp	Ser	Asp	Ser	Glu	Leu	Leu	Leu	Asn	Ile	Phe	Ala	Ala	Glu	Leu	Glu
	130					135					140				
Lys	Tyr	Asn	Lys	Tyr	Arg	Val	Asn	Asn	Asp	Asp	Ile	Phe	Cys	Ala	Leu
	145					150					155				160
Glu	Gly	Val	Tyr	Lys	Arg	Cys	Arg	Gly	Gly	Tyr	Ala	Cys	Val	Gly	Met
				165					170					175	
Leu	Ala	Gly	Tyr	Gly	Leu	Phe	Gly	Phe	Arg	Asp	Pro	Asn	Gly	Ile	Arg
			180					185					190		
Pro	Leu	Leu	Phe	Gly	Glu	Arg	Val	Asn	Asp	Asp	Gly	Thr	Met	Asp	Tyr
		195					200					205			
Met	Leu	Ala	Ser	Glu	Ser	Val	Val	Leu	Lys	Ala	His	Arg	Phe	Gln	Asn
	210					215					220				
Ile	Arg	Asp	Ile	Leu	Pro	Gly	Gln	Ala	Val	Ile	Ile	Pro	Lys	Thr	Cys
	225					230					235				240
Gly	Ser	Ser	Pro	Pro	Glu	Phe	Arg	Gln	Val	Val	Pro	Ile	Glu	Ala	Tyr
				245					250					255	
Lys	Pro	Asp	Leu	Phe	Glu	Tyr	Val	Tyr	Phe	Ala	Arg	Ala	Asp	Ser	Val
			260					265					270		
Leu	Asp	Gly	Ile	Ser	Val	Tyr	His	Thr	Arg	Leu	Leu	Met	Gly	Ile	Lys
		275					280					285			
Leu	Ala	Glu	Asn	Ile	Lys	Lys	Gln	Ile	Asp	Leu	Asp	Glu	Ile	Asp	Val
	290					295					300				
Val	Val	Ser	Val	Pro	Asp	Thr	Ala	Arg	Thr	Cys	Ala	Leu	Glu	Cys	Ala
	305					310					315				320
Asn	His	Leu	Asn	Lys	Pro	Tyr	Arg	Glu	Gly	Phe	Val	Lys	Asn	Arg	Tyr
				325					330					335	
Val	Gly	Arg	Thr	Phe	Ile	Met	Pro	Asn	Gln	Lys	Glu	Arg	Val	Ser	Ser

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Val Arg Arg Lys Leu Asn Pro Met Asn Ser Glu Phe Lys Asp Lys Arg 355 360 365		
Val Leu Ile Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Lys Glu 370 375 380		
Ile Val Asn Met Ala Lys Glu Ser Gly Ala Ala Lys Val Tyr Phe Ala 385 390 395 400		
Ser Ala Ala Pro Ala Ile Arg Phe Asn His Ile Tyr Gly Ile Asp Leu 405 410 415		
Ala Asp Thr Lys Gln Leu Val Ala Tyr Asn Arg Thr Val Glu Glu Ile 420 425 430		
Thr Ala Glu Leu Gly Cys Asp Arg Val Ile Tyr Gln Ser Leu Asp Asp 435 440 445		
Leu Ile Asp Cys Cys Lys Thr Asp Ile Ile Ser Glu Phe Glu Val Gly 450 455 460		
Val Phe Thr Gly Asn Tyr Val Thr Gly Val Glu Asp Val Tyr Leu Gln 465 470 475 480		
Glu Leu Glu Arg Cys Arg Ala Leu Asn Asn Ser Asn Lys Gly Glu Ala 485 490 495		
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 <213> Ashbya gossypii

<400> 6

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Gln Leu Asp Gln Ser Thr Thr Glu Thr Tyr Val Val Cys Cys Glu Asn 20 25 30
Glu Asp Ser Leu Asn Gln Phe Leu Gln Gln Cys Trp Gln Ile Asp Glu 35 40 45
Gly Glu Lys Val Thr Asn Leu Glu Pro Leu Gly Phe Phe Thr Lys Val 50 55 60
Val Ser Arg Asp Glu Glu Asn Leu Arg Leu Asn Val Tyr Tyr Ala Lys 65 70 75 80
Ser Pro Leu Asp Ala Gln Thr Leu Gln Phe Leu Gly Val Phe Leu Arg 85 90 95
Gln Met Glu Thr Ser Gln Ile Arg Trp Ile Phe Leu Leu Asp Trp Leu 100 105 110

Leu Asp Asp Lys Arg Leu Trp Leu Arg Gln Leu Arg Asn Ser Trp Ala
 115 120 125
 Ala Leu Glu Glu Ala Gln Val Ala Pro Phe Pro Gly Gly Ala Val Val
 130 135 140
 Val Val Leu Asn Pro Ser His Val Thr Gln Leu Glu Arg Asn Thr Met
 145 150 155 160
 Val Trp Asn Ser Arg Arg Leu Asp Leu Val His Gln Thr Leu Arg Ala
 165 170 175
 Ala Cys Leu Asn Thr Gly Ser Ala Leu Val Thr Leu Asp Pro Asn Thr
 180 185 190
 Ala Arg Glu Asp Val Met His Ile Cys Ala Leu Leu Ala Gly Leu Pro
 195 200 205
 Thr Ser Arg Pro Val Ala Met Leu Ser Leu Gln Ser Leu Phe Ile Pro
 210 215 220
 His Gly Ala Asp Ser Ile Gly Lys Ile Cys Thr Ile Ala Pro Glu Phe
 225 230 235 240
 Pro Val Ala Thr Val Phe Asp Asn Asp Phe Val Ser Ser Thr Phe Glu
 245 250 255
 Ala Ala Ile Ala Pro Glu Leu Thr Pro Gly Pro Arg Val Pro Ser Asp
 260 265 270
 His Pro Trp Leu Thr Glu Pro Thr Asn Pro Pro Ser Glu Ala Thr Ala
 275 280 285
 Trp His Phe Asp Leu Gln Gly Arg Leu Ala Thr Leu Tyr Arg His Leu
 290 295 300
 Gly Asp Ser Asn Lys Ala Ile Ser Val Thr Gln His Arg Phe His Lys
 305 310 315 320
 Pro Arg Ser Glu Asp Tyr Ala Tyr Glu Phe Glu Leu Pro Ser Lys His
 325 330 335
 Pro Thr Ile Arg Asp Leu Ile Arg Ser Ala Ala Ala Asp Ser Pro Asn
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 Asp Val Ala Asp Ser Ile Asp Gly Leu Met Asp Gly Ile Val Gln Arg
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 Asn Val His
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<212> DNA

<213> *Ashbya gossypii*

<400> 7

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CCGATTACTA CAGCTACGTG CTGGATGTGA ACTTCGCGCT GCTGAGCGCC ATGAGCGCGA	180
CCGGCCTCGC GATGGGCGCC GTGAGCGGCT CCCTCGGGAG CGCGCCGGTG CTCGCGCAGT	240
GGCCGGCAGC GATCTGGGCC GTGCGCTTCC TGCGCGCCGC GGGCTATGTC GCGATAGTCC	300
TAATCCTGCC GTTCCTGTCC GTCGTCGCAT TCCTGCAGCC GCTCTGCGAG CGCGCGCTGG	360
CGCTGTTCCC GTTTGTGCGC GCGTGGGGCA TGGACGGCGT GTTCAACTTC CTGCTGCTCT	420
CCGCCGTGCT CTGGACTGTA TTCCTGGCCG TTCGCCTGCT CCGCGCCGTC TACAGACTGC	480
TGCGCTGGCT GGTCGGTCTT TTGGTCCGCC TGGCACGCCT GCTGCTGCGA GGCGCCCGTC	540
GGACGCCTGC GGCGGCCCCC GAGGAGCCCG TCTAGCGTGC GCGCGTTCTA GGCCCTGAC	600
AGCTCCTACC TGGTGCTGGC CGCCGGTAGG GCTCGCATCG TGCGGCGCAG GCCCATTGCT	660
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GTATAAATAG GTTTTCTAGA TGCGCCAAAT CCCAGCTGGG TTTACCGGCG TCTGTTCGGG	780
ATAGTTACTT GATGGATGGG TCAACTTGAG AGCTTGGGTT TAGTGTTGAC TCCTTCTCTT	840
CATAGCACGC CGAACAAAGC GCA ATG ACT TAC AGA GAC GCA GCC ACG GCA	890
Met Thr Tyr Arg Asp Ala Ala Thr Ala	
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CTG GAG CAC CTG GCG ACG TAC GCC GAG AAG GAC GGG CTG TCC GTG GAG	938
Leu Glu His Leu Ala Thr Tyr Ala Glu Lys Asp Gly Leu Ser Val Glu	
10 15 20 25	
CAG TTG ATG GAC TCC AAG ACG CGG GGC GGG TTG ACG TAC AAC GAC TTC	986
Gln Leu Met Asp Ser Lys Thr Arg Gly Gly Leu Thr Tyr Asn Asp Phe	
30 35 40	
CTG GTC TTG CCG GGC AAG ATC GAC TTC CCA TCG TCG GAG GTG GTG CTG	1034
Leu Val Leu Pro Gly Lys Ile Asp Phe Pro Ser Ser Glu Val Val Leu	
45 50 55	
TCG TCG CGC CTG ACC AAG AAG ATC ACC TTG AAC GCG CCG TTT GTG TCG	1082
Ser Ser Arg Leu Thr Lys Lys Ile Thr Leu Asn Ala Pro Phe Val Ser	
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TCG CCG ATG GAC ACG GTG ACG GAG GCC GAC ATG GCG ATC CAC ATG GCG	1130
Ser Pro Met Asp Thr Val Thr Glu Ala Asp Met Ala Ile His Met Ala	
75 80 85	
CTC CTG GGC GGC ATC GGG ATC ATC CAC CAC AAC TGC ACT GCG GAG GAG	1178
Leu Leu Gly Gly Ile Gly Ile Ile His His Asn Cys Thr Ala Glu Glu	
90 95 100 105	
CAG GCG GAG ATG GTG CGC CGG GTC AAG AAG TAC GAA AAC GGG TTC ATC	1226
Gln Ala Glu Met Val Arg Arg Val Lys Lys Tyr Glu Asn Gly Phe Ile	
110 115 120	
AAC GCC CCC GTG GTC GTG GGG CCG GAC GCG ACG GTG GCG GAC GTG CGC	1274
Asn Ala Pro Val Val Val Gly Pro Asp Ala Thr Val Ala Asp Val Arg	

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Arg Met Lys Asn Glu Phe Gly Phe Ala Gly Phe Pro Val Thr			
140	145	150	
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TCGTTCTACT GACTGCGATC AAACGATCGT GTAGACACCT TTTACTCTGA CCGCAGACGT			1436
GCAGCGCCTT TTTGGCAGGA ACATGTACTA ACACATCAGC A GAT GAT GGC AAG			1489
	Asp Asp Gly Lys		
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CCG ACC GGG AAG CTG CAG GGG ATC ATC ACG TCC CGT GAC ATC CAG TTT			1537
Pro Thr Gly Lys Leu Gln Gly Ile Ile Thr Ser Arg Asp Ile Gln Phe			
5	10	15	20
GTC GAG GAC GAG ACC CTG CTT GTG TCT GAG ATC ATG ACC AAG GAC GTC			1585
Val Glu Asp Glu Thr Leu Leu Val Ser Glu Ile Met Thr Lys Asp Val			
	25	30	35
ATC ACT GGG AAG CAG GGC ATC AAC CTC GAG GAG GCG AAC CAG ATC CTG			1633
Ile Thr Gly Lys Gln Gly Ile Asn Leu Glu Glu Ala Asn Gln Ile Leu			
	40	45	50
AAG AAC ACC AAG AAG GGC AAG CTG CCA ATT GTG GAC GAG GCG GGC TGC			1681
Lys Asn Thr Lys Lys Gly Lys Leu Pro Ile Val Asp Glu Ala Gly Cys			
	55	60	65
CTG GTG TCC ATG CTT TCG AGA ACT GAC TTG ATG AAG AAC CAG TCC TAC			1729
Leu Val Ser Met Leu Ser Arg Thr Asp Leu Met Lys Asn Gln Ser Tyr			
	70	75	80
CCA TTG GCC TCC AAG TCT GCC GAC ACC AAG CAG CTG CTC TGT GGT GCT			1777
Pro Leu Ala Ser Lys Ser Ala Asp Thr Lys Gln Leu Leu Cys Gly Ala			
85	90	95	100
GCG ATC GGC ACC ATC GAC GCG GAC AGG CAG AGA CTG GCG ATG CTG GTC			1825
Ala Ile Gly Thr Ile Asp Ala Asp Arg Gln Arg Leu Ala Met Leu Val			
	105	110	115
GAG GCC GGT CTG GAC GTT GTT GTG CTA GAC TCC TCG CAG GGT AAC TCG			1873
Glu Ala Gly Leu Asp Val Val Val Leu Asp Ser Ser Gln Gly Asn Ser			
	120	125	130
GTC TTC CAG ATC AAC ATG ATC AAG TGG ATC AAG GAG ACC TTC CCA GAC			1921
Val Phe Gln Ile Asn Met Ile Lys Trp Ile Lys Glu Thr Phe Pro Asp			
	135	140	145
CTG CAG GTC ATT GCT GGC AAC GTG GTC ACC AGA GAG CAG GCT GCC AGC			1969
Leu Gln Val Ile Ala Gly Asn Val Val Thr Arg Glu Gln Ala Ala Ser			
	150	155	160
TTG ATC CAC GCC GGC GCA GAC GGG TTG CGT ATC GGT ATG GGC TCT GGC			2017
Leu Ile His Ala Gly Ala Asp Gly Leu Arg Ile Gly Met Gly Ser Gly			
165	170	175	180
TCC ATC TGT ATC ACT CAG GAG GTG ATG GCC TGT GGT AGA CCA CAG GGT			2065
Ser Ile Cys Ile Thr Gln Glu Val Met Ala Cys Gly Arg Pro Gln Gly			

	185	190	195	
ACC GCT GTC TAC AAC GTC ACG CAG TTC GCC AAC CAG TTT GGT GTG CCA				2113
Thr Ala Val Tyr Asn Val Thr Gln Phe Ala Asn Gln Phe Gly Val Pro				
	200	205	210	
TGT ATT GCT GAC GGT GGT GTC CAG AAC ATC GGG CAC ATT ACC AAA GCT				2161
Cys Ile Ala Asp Gly Gly Val Gln Asn Ile Gly His Ile Thr Lys Ala				
	215	220	225	
ATC GCT CTT GGC GCG TCC ACC GTC ATG ATG GGC GGT ATG CTG GCA GGC				2209
Ile Ala Leu Gly Ala Ser Thr Val Met Met Gly Gly Met Leu Ala Gly				
	230	235	240	
ACT ACA GAG TCT CCA GGC GAG TAC TTC TTC AGG GAC GGG AAG AGA CTG				2257
Thr Thr Glu Ser Pro Gly Glu Tyr Phe Phe Arg Asp Gly Lys Arg Leu				
	245	250	255	260
AAG ACC TAC AGA GGT ATG GGC TCC ATC GAC GCC ATG CAA AAG ACT GAT				2305
Lys Thr Tyr Arg Gly Met Gly Ser Ile Asp Ala Met Gln Lys Thr Asp				
	265	270	275	
GTC AAG GGT AAC GCC GCT ACC TCC CGT TAC TTC TCT GAG TCT GAC AAG				2353
Val Lys Gly Asn Ala Ala Thr Ser Arg Tyr Phe Ser Glu Ser Asp Lys				
	280	285	290	
GTT CTG GTC GCT CAG GGT GTT ACT GGT TCT GTG ATC GAC AAG GGC TCC				2401
Val Leu Val Ala Gln Gly Val Thr Gly Ser Val Ile Asp Lys Gly Ser				
	295	300	305	
ATC AAG AAG TAC ATT CCA TAT CTG TAC AAT GGT CTA CAG CAC TCG TGC				2449
Ile Lys Lys Tyr Ile Pro Tyr Leu Tyr Asn Gly Leu Gln His Ser Cys				
	310	315	320	
CAG GAT ATC GGT GTG CGC TCT CTA GTG GAG TTC AGA GAG AAG GTG GAC				2497
Gln Asp Ile Gly Val Arg Ser Leu Val Glu Phe Arg Glu Lys Val Asp				
	325	330	335	340
TCT GGC TCG GTC AGA TTT GAG TTC AGA ACT CCA TCT GCC CAG TTG GAG				2545
Ser Gly Ser Val Arg Phe Glu Phe Arg Thr Pro Ser Ala Gln Leu Glu				
	345	350	355	
GGT GGT GTG CAC AAC TTG CAC TCC TAC GAG AAG CGC CTA TTT GACTGAGTGC				2597
Gly Gly Val His Asn Leu His Ser Tyr Glu Lys Arg Leu Phe Asp				
	360	365	370	
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TTGATTGAT GTACGTAAAC GATAGATATA ATAACAGACG CGGCATCTCA TTTGTATGCA				2717
ATATATCTGG AACATGGTTA TGCGTACTCA ACTGTATGTA CTACTTTATA TACACAGCTC				2777
TGGGACACTT GGTGAGATAT ATGTTTCATT ATGTATGCCT CGCTATCGAA AGGTCTGGCA				2837
TTATGGGCTA CTGGGTCTAA GAGTCATGGC TTATGAGTAT TTATTTATTT ATTTCTCTTC				2897
CTTTTCATTA AACTCCTCGA GCTTCTTTCT GTAATACTGC TCTCTAGACT TCTCCACATC				2957
TGCTAATGAT GGTGGAAGTC GTTCGTTTTT CAAATCCGCT CTACGAGCGC GCTCGAAGTT				3017

AGACAGCGCC TCGTTCAGAC CTTCAGACCC GCGTGACAGC GCTCCACGAG GCAGCAGGCC 3077
 AGAATTCATT GTTTTTAGGT ACTGCACCTT ATCGCTCTCT TCTCTCAACA CGCTATACAT 3137
 TCGGGAAACC TTGGCAATCG CCAATATTTT ACTGCGTAGT GCACGCCGTT TTGCATCATC 3197
 GTCCAGAATA GACCGTTTTT TCTTCGATTT CTTGGAGCCA GGTATAACAG TTACAACCTG 3257
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<213> Ashbya gossypii

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 Ile His His Asn Cys Thr Ala Glu Glu Gln Ala Glu Met Val Arg Arg
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 Val Lys Lys Tyr Glu Asn Gly Phe Ile Asn Ala Pro Val Val Val Gly
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		20						25					30			
Thr	Lys	Asp	Val	Ile	Thr	Gly	Lys	Gln	Gly	Ile	Asn	Leu	Glu	Glu	Ala	
		35					40					45				
Asn	Gln	Ile	Leu	Lys	Asn	Thr	Lys	Lys	Gly	Lys	Leu	Pro	Ile	Val	Asp	
	50					55					60					
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65					70					75					80	
Asn	Gln	Ser	Tyr	Pro	Leu	Ala	Ser	Lys	Ser	Ala	Asp	Thr	Lys	Gln	Leu	
				85					90					95		
Leu	Cys	Gly	Ala	Ala	Ile	Gly	Thr	Ile	Asp	Ala	Asp	Arg	Gln	Arg	Leu	
			100					105					110			
Ala	Met	Leu	Val	Glu	Ala	Gly	Leu	Asp	Val	Val	Val	Leu	Asp	Ser	Ser	
		115					120					125				
Gln	Gly	Asn	Ser	Val	Phe	Gln	Ile	Asn	Met	Ile	Lys	Trp	Ile	Lys	Glu	
	130					135					140					
Thr	Phe	Pro	Asp	Leu	Gln	Val	Ile	Ala	Gly	Asn	Val	Val	Thr	Arg	Glu	
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Gln	Ala	Ala	Ser	Leu	Ile	His	Ala	Gly	Ala	Asp	Gly	Leu	Arg	Ile	Gly	
				165					170					175		
Met	Gly	Ser	Gly	Ser	Ile	Cys	Ile	Thr	Gln	Glu	Val	Met	Ala	Cys	Gly	
			180					185					190			
Arg	Pro	Gln	Gly	Thr	Ala	Val	Tyr	Asn	Val	Thr	Gln	Phe	Ala	Asn	Gln	
		195					200					205				
Phe	Gly	Val	Pro	Cys	Ile	Ala	Asp	Gly	Gly	Val	Gln	Asn	Ile	Gly	His	
	210					215					220					
Ile	Thr	Lys	Ala	Ile	Ala	Leu	Gly	Ala	Ser	Thr	Val	Met	Met	Gly	Gly	
225					230					235					240	
Met	Leu	Ala	Gly	Thr	Thr	Glu	Ser	Pro	Gly	Glu	Tyr	Phe	Phe	Arg	Asp	
				245					250					255		
Gly	Lys	Arg	Leu	Lys	Thr	Tyr	Arg	Gly	Met	Gly	Ser	Ile	Asp	Ala	Met	
			260					265					270			
Gln	Lys	Thr	Asp	Val	Lys	Gly	Asn	Ala	Ala	Thr	Ser	Arg	Tyr	Phe	Ser	
		275					280						285			

Glu Ser Asp Lys Val Leu Val Ala Gln Gly Val Thr Gly Ser Val Ile
 290 295 300
 Asp Lys Gly Ser Ile Lys Lys Tyr Ile Pro Tyr Leu Tyr Asn Gly Leu
 305 310 315 320
 Gln His Ser Cys Gln Asp Ile Gly Val Arg Ser Leu Val Glu Phe Arg
 325 330 335
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<400> 10

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TTATAACCAGC	AGGGATCAGC	GCAGGCACTA	GAGTGGCGGG	TGCTAATAAG	AGGAGCAGGT	180	
CCTGGAAGT	AAGTTGCAAG	AGATAAGCAT	TGCGCGGAGA	AGGAGGCGGT	TAGAGGGTGC	240	
AAGCGAGCAG	GATGGGGTCT	TCGATGAACT	TCCCGTCTGG	GTATGTGAAC	AAGCACACGC	300	
TGCAGGCACA	CCGGTAGGGC	GAGTGCAGGG	TGAAAAATAT	ATATGCGCTC	GAGAAGCGCT	360	
GGGGATGAGT	TCGTCTGCAA	CGGCAGGCGG	ATCTTCATCT	GACAAAACCA	GCTGCCTACA	420	
TCAGTGC	GAA GCTGTT	CAGT GATAGA	AATAG GAGTA	ATG GCT	GCT GTT	GAA CAA	473
				Met	Ala Ala	Val Glu Gln	
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GTT TCT AGC	GTG TTT GAC	ACC ATT TTG	GTG CTG GAC	TTC GGG TCC	CAG	521	
Val Ser Ser	Val Phe Asp	Thr Ile Leu	Val Leu Asp	Phe Gly Ser	Gln		
	10		15		20		
TAC TCG CAT	CTG ATC ACG	CGG CGG CTG	CGT GAG TTT	AAT GTG TAC	GCG	569	
Tyr Ser His	Leu Ile Thr	Arg Arg Leu	Arg Glu Phe	Asn Val Tyr	Ala		
	25		30		35		
GAG ATG CTT	CCG TGT ACG	CAG AAG ATC	AGC GAG CTG	GGC TGG AAG	CCA	617	
Glu Met Leu	Pro Cys Thr	Gln Lys Ile	Ser Glu Leu	Gly Trp Lys	Pro		
	40		45		50		
AAG GGT GTG	ATT TTG TCA	GGC GGG CCG	TAC TCC GTG	TAC GCG GCA	GAT	665	
Lys Gly Val	Ile Leu Ser	Gly Gly Pro	Tyr Ser Val	Tyr Ala Ala	Asp		
	55		60		65	70	
GCT CCG CAC	GTG GAC CGG	GCG GTG TTC	GAG TTG GGC	GTT CCA ATT	CTG	713	

Ala	Pro	His	Val	Asp	Arg	Ala	Val	Phe	Glu	Leu	Gly	Val	Pro	Ile	Leu	
				75					80					85		
GGC	ATC	TGC	TAC	GGG	CTA	CAG	GAG	CTT	GCG	TGG	ATA	GCC	GGC	GCA	GAG	761
Gly	Ile	Cys	Tyr	Gly	Leu	Gln	Glu	Leu	Ala	Trp	Ile	Ala	Gly	Ala	Glu	
			90					95					100			
GTG	GGG	CGC	GGC	GAG	AAG	CGC	GAG	TAC	GGG	CGC	GCG	ACG	CTG	CAC	GTG	809
Val	Gly	Arg	Gly	Glu	Lys	Arg	Glu	Tyr	Gly	Arg	Ala	Thr	Leu	His	Val	
		105					110					115				
GAG	GAC	AGC	GCG	TGC	CCG	CTG	TTC	AAC	AAC	GTG	GAC	AGC	AGC	ACG	GTG	857
Glu	Asp	Ser	Ala	Cys	Pro	Leu	Phe	Asn	Asn	Val	Asp	Ser	Ser	Thr	Val	
	120					125					130					
TGG	ATG	TCG	CAC	GGT	GAC	AAG	CTG	CAC	GCA	CTA	CCT	GCG	GAT	TTC	CAC	905
Trp	Met	Ser	His	Gly	Asp	Lys	Leu	His	Ala	Leu	Pro	Ala	Asp	Phe	His	
135					140					145					150	
GTC	ACT	GCG	ACG	ACG	GAG	AAC	TCT	CCT	TTC	TGC	GGG	ATT	GCA	CAC	GAC	953
Val	Thr	Ala	Thr	Thr	Glu	Asn	Ser	Pro	Phe	Cys	Gly	Ile	Ala	His	Asp	
				155					160					165		
TCG	AAG	CCA	ATC	TTC	GGG	ATC	CAG	TTC	CAC	CCT	GAG	GTG	ACG	CAC	TCC	1001
Ser	Lys	Pro	Ile	Phe	Gly	Ile	Gln	Phe	His	Pro	Glu	Val	Thr	His	Ser	
			170					175					180			
TCG	CAG	GGG	AAG	ACG	TTG	CTG	AAG	AAC	TTT	GCG	GTG	GAG	ATC	TGC	CAG	1049
Ser	Gln	Gly	Lys	Thr	Leu	Leu	Lys	Asn	Phe	Ala	Val	Glu	Ile	Cys	Gln	
		185					190					195				
GCC	GCG	CAG	ACC	TGG	ACG	ATG	GAA	AAC	TTC	ATT	GAC	ACC	GAG	ATC	CAG	1097
Ala	Ala	Gln	Thr	Trp	Thr	Met	Glu	Asn	Phe	Ile	Asp	Thr	Glu	Ile	Gln	
	200					205					210					
CGG	ATC	CGG	ACC	CTT	GTG	GGC	CCC	ACC	GCG	GAA	GTG	ATC	GGT	GCT	GTG	1145
Arg	Ile	Arg	Thr	Leu	Val	Gly	Pro	Thr	Ala	Glu	Val	Ile	Gly	Ala	Val	
215					220					225					230	
TCC	GGC	GGT	GTC	GAC	TCG	ACC	GTC	GCT	GCG	AAG	CTG	ATG	ACC	GAG	GCC	1193
Ser	Gly	Gly	Val	Asp	Ser	Thr	Val	Ala	Ala	Lys	Leu	Met	Thr	Glu	Ala	
				235					240					245		
ATC	GGC	GAC	CGG	TTC	CAC	GCG	ATC	CTG	GTC	GAC	AAC	GGT	GTT	CTG	CGC	1241
Ile	Gly	Asp	Arg	Phe	His	Ala	Ile	Leu	Val	Asp	Asn	Gly	Val	Leu	Arg	
		250						255					260			
CTC	AAC	GAA	GCG	GCC	AAT	GTG	AAG	AAA	ATC	CTC	GGC	GAG	GGC	TTG	GGC	1289
Leu	Asn	Glu	Ala	Ala	Asn	Val	Lys	Lys	Ile	Leu	Gly	Glu	Gly	Leu	Gly	
		265					270					275				
ATC	AAC	TTG	ACT	GTT	GTT	GAC	GCC	TCC	GAA	GAG	TTC	TTG	ACG	AAG	CTC	1337
Ile	Asn	Leu	Thr	Val	Val	Asp	Ala	Ser	Glu	Glu	Phe	Leu	Thr	Lys	Leu	
	280					285					290					
AAG	GGC	GTC	ACG	GAC	CCT	GAG	AAG	AAG	AGA	AAG	ATC	ATC	GGT	AAC	ACC	1385
Lys	Gly	Val	Thr	Asp	Pro	Glu	Lys	Lys	Arg	Lys	Ile	Ile	Gly	Asn	Thr	
295					300					305					310	
TTC	ATT	CAT	GTT	TTT	GAG	CGC	GAG	GCA	GCC	AGG	ATC	CAG	CCT	AAG	AAC	1433

Phe	Ile	His	Val	Phe	Glu	Arg	Glu	Ala	Ala	Arg	Ile	Gln	Pro	Lys	Asn	
				315					320					325		
GGC	GAG	GAG	ATT	GAG	TTC	CTG	TTG	CAG	GGT	ACC	CTA	TAC	CCT	GAC	GTT	1481
Gly	Glu	Glu	Ile	Glu	Phe	Leu	Leu	Gln	Gly	Thr	Leu	Tyr	Pro	Asp	Val	
			330					335					340			
ATC	GAG	TCC	ATT	TCC	TTT	AAG	GGC	CCA	TCT	CAG	ACG	ATC	AAG	ACC	CAC	1529
Ile	Glu	Ser	Ile	Ser	Phe	Lys	Gly	Pro	Ser	Gln	Thr	Ile	Lys	Thr	His	
			345				350					355				
CAT	AAC	GTC	GGT	GGT	CTT	TTG	GAC	AAC	ATG	AAA	CTG	AAG	CTC	ATT	GAG	1577
His	Asn	Val	Gly	Gly	Leu	Leu	Asp	Asn	Met	Lys	Leu	Lys	Leu	Ile	Glu	
			360				365				370					
CCT	TTG	CGC	GAG	CTT	TTC	AAG	GAC	GAG	GTG	AGA	CAC	CTG	GGA	GAA	CTA	1625
Pro	Leu	Arg	Glu	Leu	Phe	Lys	Asp	Glu	Val	Arg	His	Leu	Gly	Glu	Leu	
					380					385					390	
TTG	GGG	ATC	TCC	CAC	GAG	TTG	GTC	TGG	AGA	CAT	CCG	TTC	CCA	GGC	CCA	1673
Leu	Gly	Ile	Ser	His	Glu	Leu	Val	Trp	Arg	His	Pro	Phe	Pro	Gly	Pro	
				395				400						405		
GGT	ATC	GCC	ATC	CGT	GTG	CTA	GGC	GAG	GTC	ACC	AAG	GAG	CAG	GTG	GAG	1721
Gly	Ile	Ala	Ile	Arg	Val	Leu	Gly	Glu	Val	Thr	Lys	Glu	Gln	Val	Glu	
			410					415					420			
ATT	GCC	AGA	AAG	GCA	GAC	CAC	ATC	TAC	ATC	GAG	GAG	ATC	AGG	AAA	GCA	1769
Ile	Ala	Arg	Lys	Ala	Asp	His	Ile	Tyr	Ile	Glu	Glu	Ile	Arg	Lys	Ala	
			425				430					435				
GGT	CTA	TAC	AAC	AAG	ATT	TCT	CAA	GCT	TTT	GCT	TGC	TTG	CTG	CCT	GTT	1817
Gly	Leu	Tyr	Asn	Lys	Ile	Ser	Gln	Ala	Phe	Ala	Cys	Leu	Leu	Pro	Val	
			440				445				450					
AAG	TCT	GTG	GGT	GTC	ATG	GGT	GAC	CAG	AGA	ACC	TAC	GAC	CAG	GTC	ATT	1865
Lys	Ser	Val	Gly	Val	Met	Gly	Asp	Gln	Arg	Thr	Tyr	Asp	Gln	Val	Ile	
					460					465					470	
GCT	CTA	AGA	GCA	ATT	GAG	ACC	ACG	GAC	TTC	ATG	ACT	GCC	GAC	TGG	TAT	1913
Ala	Leu	Arg	Ala	Ile	Glu	Thr	Thr	Asp	Phe	Met	Thr	Ala	Asp	Trp	Tyr	
				475						480				485		
CCA	TTT	GAG	CAC	GAA	TTC	TTG	AAG	CAT	GTC	GCA	TCC	CGT	ATT	GTT	AAC	1961
Pro	Phe	Glu	His	Glu	Phe	Leu	Lys	His	Val	Ala	Ser	Arg	Ile	Val	Asn	
			490					495					500			
GAG	GTT	GAA	GGT	GTT	GCC	AGA	GTC	ACC	TAC	GAC	ATA	ACT	TCT	AAG	CCT	2009
Glu	Val	Glu	Gly	Val	Ala	Arg	Val	Thr	Tyr	Asp	Ile	Thr	Ser	Lys	Pro	
			505				510					515				
CCA	GCT	ACC	GTT	GAA	TGG	GAA	TAATCACCCT	TGGGATCCGC	TGACTGGCTA							2060
Pro	Ala	Thr	Val	Glu	Trp	Glu	</									

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 Glu Leu Gly Trp Lys Pro Lys Gly Val Ile Leu Ser Gly Gly Pro Tyr
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 Ser Val Tyr Ala Ala Asp Ala Pro His Val Asp Arg Ala Val Phe Glu
 65 70 75 80
 Leu Gly Val Pro Ile Leu Gly Ile Cys Tyr Gly Leu Gln Glu Leu Ala
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 Trp Ile Ala Gly Ala Glu Val Gly Arg Gly Glu Lys Arg Glu Tyr Gly
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 Arg Ala Thr Leu His Val Glu Asp Ser Ala Cys Pro Leu Phe Asn Asn
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 Val Asp Ser Ser Thr Val Trp Met Ser His Gly Asp Lys Leu His Ala
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 Leu Pro Ala Asp Phe His Val Thr Ala Thr Thr Glu Asn Ser Pro Phe
 145 150 155 160
 Cys Gly Ile Ala His Asp Ser Lys Pro Ile Phe Gly Ile Gln Phe His
 165 170 175
 Pro Glu Val Thr His Ser Ser Gln Gly Lys Thr Leu Leu Lys Asn Phe
 180 185 190

Ala	Val	Glu	Ile	Cys	Gln	Ala	Ala	Gln	Thr	Trp	Thr	Met	Glu	Asn	Phe	195	200	205	
Ile	Asp	Thr	Glu	Ile	Gln	Arg	Ile	Arg	Thr	Leu	Val	Gly	Pro	Thr	Ala	210	215	220	
Glu	Val	Ile	Gly	Ala	Val	Ser	Gly	Gly	Val	Asp	Ser	Thr	Val	Ala	Ala	225	230	235	240
Lys	Leu	Met	Thr	Glu	Ala	Ile	Gly	Asp	Arg	Phe	His	Ala	Ile	Leu	Val	245	250	255	
Asp	Asn	Gly	Val	Leu	Arg	Leu	Asn	Glu	Ala	Ala	Asn	Val	Lys	Lys	Ile	260	265	270	
Leu	Gly	Glu	Gly	Leu	Gly	Ile	Asn	Leu	Thr	Val	Val	Asp	Ala	Ser	Glu	275	280	285	
Glu	Phe	Leu	Thr	Lys	Leu	Lys	Gly	Val	Thr	Asp	Pro	Glu	Lys	Lys	Arg	290	295	300	
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Arg	Ile	Gln	Pro	Lys	Asn	Gly	Glu	Glu	Ile	Glu	Phe	Leu	Leu	Gln	Gly	325	330	335	
Thr	Leu	Tyr	Pro	Asp	Val	Ile	Glu	Ser	Ile	Ser	Phe	Lys	Gly	Pro	Ser	340	345	350	
Gln	Thr	Ile	Lys	Thr	His	His	Asn	Val	Gly	Gly	Leu	Leu	Asp	Asn	Met	355	360	365	
Lys	Leu	Lys	Leu	Ile	Glu	Pro	Leu	Arg	Glu	Leu	Phe	Lys	Asp	Glu	Val	370	375	380	
Arg	His	Leu	Gly	Glu	Leu	Leu	Gly	Ile	Ser	His	Glu	Leu	Val	Trp	Arg	385	390	395	400
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Glu	Glu	Ile	Arg	Lys	Ala	Gly	Leu	Tyr	Asn	Lys	Ile	Ser	Gln	Ala	Phe	435	440	445	
Ala	Cys	Leu	Leu	Pro	Val	Lys	Ser	Val	Gly	Val	Met	Gly	Asp	Gln	Arg	450	455	460	
Thr	Tyr	Asp	Gln	Val	Ile	Ala	Leu	Arg	Ala	Ile	Glu	Thr	Thr	Asp	Phe	465	470	475	480
Met	Thr	Ala	Asp	Trp	Tyr	Pro	Phe	Glu	His	Glu	Phe	Leu	Lys	His	Val	485	490	495	
Ala	Ser	Arg	Ile	Val	Asn	Glu	Val	Glu	Gly	Val	Ala	Arg	Val	Thr	Tyr	500	505	510	

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ATGTTACGGG ATGTCCCTGA CGCCACAGAA GGTAGCCTGG TGGTCCAGAC AGAAAAAGAG	180
CCTACACCAA AGAAGAAACA TAACAAGAAA AAGCCTCCGC ATCGTTTTGG TAAATCATAA	240
TAGGCACGAT GCGCATATAC CCTGACCATC ATAGCGGTTC CCCCCGCTAA CTGCTCCGAG	300
CGGGTAACCC CATGTCACAA AGTGA CTCTG TCTCTTCGTG GTAGGTGATG TCAAATTTTC	360
ACGACTTCCC ACCCCGATGA GCATCCGTAT TCCTTTTCAT CTAAATTCTA ATAGATGGCT	420
TATGGATTCT TATTGGCGAC TTACAAGCCT ATGTAGTTGG CTTCCCTCAA GTGTTCGTAG	480
TCTACCACCT CACACCCGGT CTAACAGCTT ACGAGAATA ATG GCT ACT AAT GCA	534
Met Ala Thr Asn Ala	
1 5	
ATC AAG CTT CTT GCG CCA GAT ATC CAC AGG GGT CTG GCA GAG CTG GTC	582
Ile Lys Leu Leu Ala Pro Asp Ile His Arg Gly Leu Ala Glu Leu Val	
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GCT AAA CGC CTA GGC TTA CGT CTG ACA GAC TGC AAG CTT AAG CGG GAT	630
Ala Lys Arg Leu Gly Leu Arg Leu Thr Asp Cys Lys Leu Lys Arg Asp	
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TGT AAC GGG GAG GCG ACA TTT TCG ATC GGA GAA TCT GTT CGA GAC CAG	678
Cys Asn Gly Glu Ala Thr Phe Ser Ile Gly Glu Ser Val Arg Asp Gln	
40 45 50	
GAT ATC TAC ATC ATC ACG CAG GTG GGG TCC GGG GAC GTG AAC GAC CGA	726
Asp Ile Tyr Ile Ile Thr Gln Val Gly Ser Gly Asp Val Asn Asp Arg	
55 60 65	
GTG CTG GAG CTG CTC ATC ATG ATC AAC GCT AGC AAG ACG GCG TCT GCG	774
Val Leu Glu Leu Leu Ile Met Ile Asn Ala Ser Lys Thr Ala Ser Ala	
70 75 80 85	
CGG CGA ATT ACG GCT GTG ATT CCA AAC TTC CCA TAC GCG CGG CAG GAC	822
Arg Arg Ile Thr Ala Val Ile Pro Asn Phe Pro Tyr Ala Arg Gln Asp	
90 95 100	
CGG AAG GAT AAG TCA CGG GCG CCA ATT ACC GCG AAG CTC ATG GCG GAC	870
Arg Lys Asp Lys Ser Arg Ala Pro Ile Thr Ala Lys Leu Met Ala Asp	
105 110 115	
ATG CTG ACT ACC GCG GGC TGC GAT CAT GTC ATC ACC ATG GAC TTA CAC	918
Met Leu Thr Thr Ala Gly Cys Asp His Val Ile Thr Met Asp Leu His	

120	125	130	
GCT TCG CAA ATC CAG GGC TTC TTT GAT GTA CCA GTT GAC AAC CTT TAC			966
Ala Ser Gln Ile Gln Gly Phe Phe Asp Val Pro Val Asp Asn Leu Tyr			
135	140	145	
GCA GAG CCT AGC GTG GTG AAG TAT ATC AAG GAG CAT ATT CCC CAC GAC			1014
Ala Glu Pro Ser Val Val Lys Tyr Ile Lys Glu His Ile Pro His Asp			
150	155	160	165
GAT GCC ATC ATC ATC TCG CCG GAT GCT GGT GGT GCC AAA CGT GCG TCG			1062
Asp Ala Ile Ile Ile Ser Pro Asp Ala Gly Gly Ala Lys Arg Ala Ser			
170	175	180	
CTT CTA TCA GAT CGC CTA AAC TTG AAC TTT GCG CTG ATT CAT AAG GAA			1110
Leu Leu Ser Asp Arg Leu Asn Leu Asn Phe Ala Leu Ile His Lys Glu			
185	190	195	
CGT GCA AAG GCA AAC GAA GTG TCC CGC ATG GTT CTG GTC GGC GAT GTT			1158
Arg Ala Lys Ala Asn Glu Val Ser Arg Met Val Leu Val Gly Asp Val			
200	205	210	
ACC GAT AAA GTC TGC ATT ATC GTT GAC GAT ATG GCG GAT ACT TGT GGT			1206
Thr Asp Lys Val Cys Ile Ile Val Asp Asp Met Ala Asp Thr Cys Gly			
215	220	225	
ACG CTG GCC AAG GCG GCA GAA GTG CTG CTA GAG CAC AAC GCG CGG TCT			1254
Thr Leu Ala Lys Ala Ala Glu Val Leu Leu Glu His Asn Ala Arg Ser			
230	235	240	245
GTG ATA GCC ATT GTT ACC CAC GGT ATC CTT TCA GGA AAG GCC ATT GAG			1302
Val Ile Ala Ile Val Thr His Gly Ile Leu Ser Gly Lys Ala Ile Glu			
250	255	260	
AAC ATC AAC AAT TCG AAG CTT GAT AGG GTT GTG TGT ACC AAC ACC GTG			1350
Asn Ile Asn Asn Ser Lys Leu Asp Arg Val Val Cys Thr Asn Thr Val			
265	270	275	
CCA TTC GAG GAG AAG ATG AAG TTA TGC CCG AAG TTA GAT GTA ATT GAT			1398
Pro Phe Glu Glu Lys Met Lys Leu Cys Pro Lys Leu Asp Val Ile Asp			
280	285	290	
ATC TCG GCA GTT CTT GCG GAA TCC ATT CGC CGT CTA CAC AAT GGT GAA			1446
Ile Ser Ala Val Leu Ala Glu Ser Ile Arg Arg Leu His Asn Gly Glu			
295	300	305	
AGT ATC TCC TAC CTC TTT AAA AAC AAC CCA CTA TGATTTTGCT TCTCGATGCT			1499
Ser Ile Ser Tyr Leu Phe Lys Asn Asn Pro Leu			
310	315	320	
GGCTTCTTGA GGGCCAATTT TGCCGTAGAG GTAGTATCCC TTCTTTTAT ATTGACTATT			1559
TAACGAAGAC TATTTCTTCA TAAATGGACT TCGGCTTCAC TGTGAATCTC ACATGATATA			1619
GTTGTTTCAG AGACC			1634

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<213> Ashbya gossypii

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Leu Ala Glu Leu Val Ala Lys Arg Leu Gly Leu Arg Leu Thr Asp Cys
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Lys Leu Lys Arg Asp Cys Asn Gly Glu Ala Thr Phe Ser Ile Gly Glu
35 40 45
Ser Val Arg Asp Gln Asp Ile Tyr Ile Ile Thr Gln Val Gly Ser Gly
50 55 60
Asp Val Asn Asp Arg Val Leu Glu Leu Leu Ile Met Ile Asn Ala Ser
65 70 75 80
Lys Thr Ala Ser Ala Arg Arg Ile Thr Ala Val Ile Pro Asn Phe Pro
85 90 95
Tyr Ala Arg Gln Asp Arg Lys Asp Lys Ser Arg Ala Pro Ile Thr Ala
100 105 110
Lys Leu Met Ala Asp Met Leu Thr Thr Ala Gly Cys Asp His Val Ile
115 120 125
Thr Met Asp Leu His Ala Ser Gln Ile Gln Gly Phe Phe Asp Val Pro
130 135 140
Val Asp Asn Leu Tyr Ala Glu Pro Ser Val Val Lys Tyr Ile Lys Glu
145 150 155 160
His Ile Pro His Asp Asp Ala Ile Ile Ile Ser Pro Asp Ala Gly Gly
165 170 175
Ala Lys Arg Ala Ser Leu Leu Ser Asp Arg Leu Asn Leu Asn Phe Ala
180 185 190
Leu Ile His Lys Glu Arg Ala Lys Ala Asn Glu Val Ser Arg Met Val
195 200 205
Leu Val Gly Asp Val Thr Asp Lys Val Cys Ile Ile Val Asp Asp Met
210 215 220
Ala Asp Thr Cys Gly Thr Leu Ala Lys Ala Ala Glu Val Leu Leu Glu
225 230 235 240
His Asn Ala Arg Ser Val Ile Ala Ile Val Thr His Gly Ile Leu Ser
245 250 255
Gly Lys Ala Ile Glu Asn Ile Asn Asn Ser Lys Leu Asp Arg Val Val
260 265 270
Cys Thr Asn Thr Val Pro Phe Glu Glu Lys Met Lys Leu Cys Pro Lys
275 280 285
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Leu His Asn Gly Glu Ser Ile Ser Tyr Leu Phe Lys Asn Asn Pro Leu
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